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JUN 14 2002
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RAW SEQUENCE LISTING

DATE: 05/02/2002

PATENT APPLICATION: US/09/218,913D

TIME: 13:57:40

Input Set : A:\09-218,913 sequence listing.txt

Output Set: N:\CRF3\05022002\I218913D.raw

p.6

ENTERED

3 <110> APPLICANT: Hall, Roderick L.
 4 Poll, Christopher T.
 5 Newton, Benjamin B.
 6 Taylor, William J.A.
 8 <120> TITLE OF INVENTION: Method For Accelerating The Rate of Mucociliary Clearance
 10 <130> FILE REFERENCE: 98-736
 12 <140> CURRENT APPLICATION NUMBER: US 09/218,913D
 13 <141> CURRENT FILING DATE: 1998-12-22
 15 <160> NUMBER OF SEQ ID NOS: 105
 17 <170> SOFTWARE: PatentIn version 3.1
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 179
 21 <212> TYPE: PRT
 22 <213> ORGANISM: Homo sapiens
 24 <400> SEQUENCE: 1
 26 Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser Lys Val
 27 1 5 10 15
 30 Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn Val Thr
 31 20 25 30
 34 Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser
 35 35 40 45
 38 Asn Asn Tyr Leu Thr Lys Glu Cys Leu Lys Lys Cys Ala Thr Val
 39 50 55 60
 42 Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp
 43 65 70 75 80
 46 Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu Asp His Ser
 47 85 90 95
 50 Ser Asp Met Phe Asn Tyr Glu Glu Tyr Cys Thr Ala Asn Ala Val Thr
 51 100 105 110
 54 Gly Pro Cys Arg Ala Ser Phe Pro Arg Trp Tyr Phe Asp Val Glu Arg
 55 115 120 125
 58 Asn Ser Cys Asn Asn Phe Ile Tyr Gly Gly Cys Arg Gly Asn Lys Asn
 59 130 135 140
 62 Ser Tyr Arg Ser Glu Glu Ala Cys Met Leu Arg Cys Phe Arg Gln Gln
 63 145 150 155 160
 66 Glu Asn Pro Pro Leu Pro Leu Gly Ser Lys Val Val Val Leu Ala Gly
 67 165 170 175
 70 Ala Val Ser
 74 <210> SEQ ID NO: 2
 75 <211> LENGTH: 197
 76 <212> TYPE: PRT
 77 <213> ORGANISM: Homo sapiens
 79 <220> FEATURE:

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80 <221> NAME/KEY: SIGNAL
81 <222> LOCATION: (1)..(18)
82 <223> OTHER INFORMATION:
85 <400> SEQUENCE: 2
87 Ala Gly Ser Phe Leu Ala Trp Leu Gly Ser Leu Leu Leu Ser Gly Val
88 1          5          10          15
91 Leu Ala Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser
92          20          25          30
95 Lys Val Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn
96          35          40          45
99 Val Thr Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly
100         50          55          60
103 Asn Ser Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala
104 65          70          75          80
107 Thr Val Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala
108          85          90          95
111 Ala Asp Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu Asp
112          100         105         110
115 His Ser Ser Asp Met Phe Asn Tyr Glu Glu Tyr Cys Thr Ala Asn Ala
116          115         120         125
119 Val Thr Gly Pro Cys Arg Ala Ser Phe Pro Arg Trp Tyr Phe Asp Val
120         130         135         140
123 Glu Arg Asn Ser Cys Asn Asn Phe Ile Tyr Gly Gly Cys Arg Gly Asn
124 145         150         155         160
127 Lys Asn Ser Tyr Arg Ser Glu Glu Ala Cys Met Leu Arg Cys Phe Arg
128          165         170         175
131 Gln Gln Glu Asn Pro Pro Leu Pro Leu Gly Ser Lys Val Val Val Leu
132          180         185         190
135 Ala Gly Ala Val Ser
136          195
139 <210> SEQ ID NO: 3
140 <211> LENGTH: 153
141 <212> TYPE: PRT
142 <213> ORGANISM: Homo sapiens
144 <400> SEQUENCE: 3
146 Ile His Asp Phe Cys Leu Val Ser Lys Val Val Gly Arg Cys Arg Ala
147 1          5          10          15
150 Ser Met Pro Arg Trp Trp Tyr Asn Val Thr Asp Gly Ser Cys Gln Leu
151          20          25          30
154 Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser Asn Asn Tyr Leu Thr Lys
155          35          40          45
158 Glu Glu Cys Leu Lys Lys Cys Ala Thr Val Thr Glu Asn Ala Thr Gly
159          50          55          60
162 Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp Ser Ser Val Pro Ser Ala
163 65          70          75          80
166 Pro Arg Arg Gln Asp Ser Glu Asp His Ser Ser Asp Met Phe Asn Tyr
167          85          90          95
170 Glu Glu Tyr Cys Thr Ala Asn Ala Val Thr Gly Pro Cys Arg Ala Ser
171         100         105         110

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```

174 Phe Pro Arg Trp Tyr Phe Asp Val Glu Arg Asn Ser Cys Asn Asn Phe
175      115      120      125
178 Ile Tyr Gly Gly Cys Arg Gly Asn Lys Asn Ser Tyr Arg Ser Glu Glu
179      130      135      140
182 Ala Cys Met Leu Arg Cys Phe Arg Gln
183 145      150
186 <210> SEQ ID NO: 4
187 <211> LENGTH: 58
188 <212> TYPE: PRT
189 <213> ORGANISM: Homo sapiens
191 <400> SEQUENCE: 4
193 Ile His Asp Phe Cys Leu Val Ser Lys Val Val Gly Arg Cys Arg Ala
194 1      5      10      15
197 Ser Met Pro Arg Trp Trp Tyr Asn Val Thr Asp Gly Ser Cys Gln Leu
198      20      25      30
201 Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser Asn Asn Tyr Leu Thr Lys
202      35      40      45
205 Glu Glu Cys Leu Lys Lys Cys Ala Thr Val
206      50      55
209 <210> SEQ ID NO: 5
210 <211> LENGTH: 51
211 <212> TYPE: PRT
212 <213> ORGANISM: Homo sapiens
214 <400> SEQUENCE: 5
216 Cys Leu Val Ser Lys Val Val Gly Arg Cys Arg Ala Ser Met Pro Arg
217 1      5      10      15
220 Trp Trp Tyr Asn Val Thr Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly
221      20      25      30
224 Gly Cys Asp Gly Asn Ser Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu
225      35      40      45
228 Lys Lys Cys
229      50
232 <210> SEQ ID NO: 6
233 <211> LENGTH: 58
234 <212> TYPE: PRT
235 <213> ORGANISM: Homo sapiens
237 <400> SEQUENCE: 6
239 Tyr Glu Glu Tyr Cys Thr Ala Asn Ala Val Thr Gly Pro Cys Arg Ala
240 1      5      10      15
243 Ser Phe Pro Arg Trp Tyr Phe Asp Val Glu Arg Asn Ser Cys Asn Asn
244      20      25      30
247 Phe Ile Tyr Gly Gly Cys Arg Gly Asn Lys Asn Ser Tyr Arg Ser Glu
248      35      40      45
251 Glu Ala Cys Met Leu Arg Cys Phe Arg Gln
252      50      55
255 <210> SEQ ID NO: 7
256 <211> LENGTH: 51
257 <212> TYPE: PRT
258 <213> ORGANISM: Homo sapiens

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260 <400> SEQUENCE: 7
262 Cys Thr Ala Asn Ala Val Thr Gly Pro Cys Arg Ala Ser Phe Pro Arg
263 1 5 10 15
266 Trp Tyr Phe Asp Val Glu Arg Asn Ser Cys Asn Asn Phe Ile Tyr Gly
267 20 25 30
270 Gly Cys Arg Gly Asn Lys Asn Ser Tyr Arg Ser Glu Glu Ala Cys Met
271 35 40 45
274 Leu Arg Cys
275 50
278 <210> SEQ ID NO: 8
279 <211> LENGTH: 92
280 <212> TYPE: PRT
281 <213> ORGANISM: Homo sapiens
283 <400> SEQUENCE: 8
285 Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser Lys Val
286 1 5 10 15
289 Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn Val Thr
290 20 25 30
293 Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser
294 35 40 45
297 Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala Thr Val
298 50 55 60
301 Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp
302 65 70 75 80
305 Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser
306 85 90
309 <210> SEQ ID NO: 9
310 <211> LENGTH: 708
311 <212> TYPE: DNA
312 <213> ORGANISM: Artificial Sequence
314 <220> FEATURE:
315 <223> OTHER INFORMATION: Consensus DNA sequence of human Bikunin (Fig. 3).
317 <220> FEATURE:
318 <221> NAME/KEY: misc_feature
319 <222> LOCATION: (679)..(679)
320 <223> OTHER INFORMATION: "n" is any nucleotide.
323 <220> FEATURE:
324 <221> NAME/KEY: misc_feature
325 <222> LOCATION: (707)..(707)
326 <223> OTHER INFORMATION: "n" is any nucleotide.
329 <400> SEQUENCE: 9
330 ggccgggtcg tttctgcct ggtggtggtc gctgctcctc tctgggggtcc tggcggccga 60
332 ccgagaacgc agcatccacg acttctgcct ggtgtcgaag gtggtgggca gatgccgggc 120
334 ctccatgcct aggtggtggt acaatgtcac tgacggatcc tgccagctgt ttgtgtatgg 180
336 gggctgtgac ggaaacagca ataattacct gaccaaggag gagtgcctca agaaatgtgc 240
338 cactgtcaca gagaatgcc a cgggtgacct ggcaccagc aggaatgcag cggattcctc 300
340 tgtcccaagt gctcccgaa ggcaggattc tgaagaccac tccagcgata tgttcaacta 360
342 tgaagaatac tgcaccgcca acgcagtcac tgggccttgc cgtgcctcct tcccacgctg 420
344 gtactttgac gtggagagga actcctgcaa taacttcac tatggaggct gccggggcaa 480

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Input Set : A:\09-218,913 sequence listing.txt

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346 taagaacagc taccgctctg aggaggcctg catgctccgc tgcttccgcc agcaggagaa 540
 348 tcctccctg ccccttggt caaaggtggt ggttctggcc ggggctgttt cgtgatggtg 600
 350 ttgatccttt tcctggggag catccatggt ctactgatt ccgggtggca aggaggaacc 660
 352 **aggagcgtgc cctgcgganc gtctggagct tcggagatga caaggnt** 708
 355 <210> SEQ ID NO: 10
 356 <211> LENGTH: 197
 357 <212> TYPE: PRT
 358 <213> ORGANISM: Artificial Sequence
 360 <220> FEATURE:
 361 <223> OTHER INFORMATION: Amino acids -18 to 179 of translation of consensus sequence
 in Fig. 3.
 363 <400> SEQUENCE: 10
 365 Ala Gly Ser Phe Leu Ala Trp Leu Gly Ser Leu Leu Leu Ser Gly Val
 366 1 5 10 15
 369 Leu Ala Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser
 370 20 25 30
 373 Lys Val Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn
 374 35 40 45
 377 Val Thr Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly
 378 50 55 60
 381 Asn Ser Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala
 382 65 70 75 80
 385 Thr Val Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala
 386 85 90 95
 389 Ala Asp Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu Asp
 390 100 105 110
 393 His Ser Ser Asp Met Phe Asn Tyr Glu Glu Tyr Cys Thr Ala Asn Ala
 394 115 120 125
 397 Val Thr Gly Pro Cys Arg Ala Ser Phe Pro Arg Trp Tyr Phe Asp Val
 398 130 135 140
 401 Glu Arg Asn Ser Cys Asn Asn Phe Ile Tyr Gly Gly Cys Arg Gly Asn
 402 145 150 155 160
 405 Lys Asn Ser Tyr Arg Ser Glu Glu Ala Cys Met Leu Arg Cys Phe Arg
 406 165 170 175
 409 Gln Gln Glu Asn Pro Pro Leu Pro Leu Gly Ser Lys Val Val Val Leu
 410 180 185 190
 413 Ala Gly Ala Val Ser
 414 195
 417 <210> SEQ ID NO: 11
 418 <211> LENGTH: 179
 419 <212> TYPE: PRT
 420 <213> ORGANISM: Artificial Sequence
 422 <220> FEATURE:
 423 <223> OTHER INFORMATION: Variants of human Bikunin.
 425 <220> FEATURE:
 426 <221> NAME/KEY: MISC_FEATURE
 427 <222> LOCATION: (8)..(8)
 428 <223> OTHER INFORMATION: Each "Xaa" independently represents a naturally occurring
 amino
 429 acid residue except Cys, with the proviso that at least one "Xaa"
 430 in SEQ ID NO:11 is different from the corresponding amino acid

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/218,913D

DATE: 05/02/2002
TIME: 13:57:41

Input Set : A:\09-218,913 sequence listing.txt
Output Set: N:\CRF3\05022002\I218913D.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; N Pos. 679,707
Seq#:11; Xaa Pos. 8,17,19,21,22,23,24,25,26,40,42,45,46,47,52,64,103,112
Seq#:11; Xaa Pos. 114,116,117,118,119,120,121,135,137,140,141,142,147,159
Seq#:12; N Pos. 361,367,384,390
Seq#:14; N Pos. 424,481,509
Seq#:16; N Pos. 3,11,12,17,48,425
Seq#:17; N Pos. 6,401,407
Seq#:48; N Pos. 1358
Seq#:51; N Pos. 46,117,313
Seq#:72; Xaa Pos. 9,11,17,19
Seq#:74; Xaa Pos. 25
Seq#:75; N Pos. 425,482,510
Seq#:76; Xaa Pos. 25
Seq#:77; N Pos. 45,49,118,231,305
Seq#:78; N Pos. 117,123,321
Seq#:79; N Pos. 9,11,222,231,262,267,274
Seq#:80; N Pos. 44,46,76,114,187,268,309,317,332,370
Seq#:81; N Pos. 35,148,235,261,272,293,300,313,320
Seq#:82; N Pos. 56,137,145,159,233
Seq#:83; N Pos. 20,26,95,292,313,314,315
Seq#:84; N Pos. 27,139,223,232,302,310,322,328,357,375,392,398,405,427,437
Seq#:84; N Pos. 449,458,474
Seq#:85; N Pos. 361,367,384,390
Seq#:86; N Pos. 3,11,12,17,48,425
Seq#:87; N Pos. 7,403,409
Seq#:88; N Pos. 48,62,211,232,245,309,318
Seq#:89; N Pos. 424,481,509
Seq#:90; N Pos. 257
Seq#:91; N Pos. 19,147
Seq#:92; N Pos. 33,55,213,228,259,267,324,333,344,387
Seq#:93; N Pos. 306,328,342,365,370,377,382,402
Seq#:94; N Pos. 1,142,339,347
Seq#:95; N Pos. 334,368,376
Seq#:96; N Pos. 108,261
Seq#:97; N Pos. 20,30
Seq#:98; N Pos. 45,102,105,159,174,213,337
Seq#:100; N Pos. 304,309
Seq#:101; N Pos. 24
Seq#:102; N Pos. 61,74,122,184
Seq#:103; N Pos. 7
Seq#:104; N Pos. 32,67,136
Seq#:105; N Pos. 13,19,107